REMARKS

Objection to the Specification

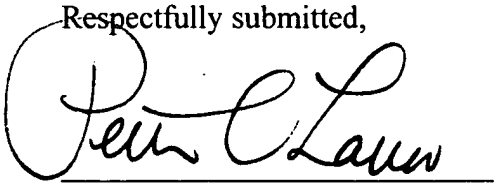
The specification is objected to because a paper copy of the sequence listing is absent, and because certain sequence disclosures appearing at pages 6, 55, 56, 98 and 101 were not assigned sequence identifiers in Applicants' response filed March 1, 2001.

Accordingly, Applicants submit herewith a computer readable form of a substitute Sequence Listing and a hard (paper) copy of the substitute Sequence Listing, both of which include all of the sequences that are present in the application. The content of the hard copy of the substitute Sequence Listing and the computer readable form of the substitute Sequence Listing are the same and include no new matter. In addition, an amendment directing entry of the hard copy of the substitute Sequence Listing into the specification is set forth above. Further, pages 6, 55, 56, 98, and 101 have been amended to insert sequence identifiers. A "marked up version" showing the amendments to specification, and a clean copy of the affected sections of the specification are attached hereto as Appendices A and B, respectively. Accordingly, Applicants respectfully request that the objections pertaining to the sequence listing be withdrawn.

SUMMARY

In light of the foregoing remarks, reconsideration of the rejections and allowance of the pending claims are respectfully requested. If a telephone conversation with Applicants' Attorney would expedite the prosecution of the above-identified application, the Examiner is urged to call the undersigned at (617) 227-7400.

Respectfully submitted,



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Dated: **June 22, 2001**

Appendix A

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Page 6 of the specification, beginning at line 1 and ending at line 9, has been amended as follows:

on expression of the transcription factor STE12. STE12 stimulates expression of a wide variety of genes involved in mating, including FUS1 (cell fusion), FAR1 (cell-cycle arrest), STE2 (the receptor), MFA1 (the pheromone), SST2 (recovery), KAR3 (nuclear fusion) and STE6 (pheromone secretion). Other genes activated by the pathway are CHS1, AGα1, and KAR3. The multiply tandem sequence TGAAACA (SEQ ID NO:128) has been recognized as a "pheromone response element" found in the 5'-flanking regions of many of the genes of this pathway.

Page 55 of the specification, beginning at line 28 and ending at line 34, has been amended as follows:

Several predictive algorithms indicate that the amino terminal domain up to the highly conserved sequence motif-LLLLGAGESG- (SEQ ID NO:129) (the first L in this motif is residue 43 in GPA1) forms a helical structure with amphipathic character. Assuming that a heptahelical repeat unit, the following hybrids between GPA1 and GaS can be used to define the number of helical repeats in this motif necessary for hybrid function:

Page 56 of the specification, beginning at line 19 and ending at line 21, has been amended as follows:

The gap that is introduced between residues 9 and 10 in the GaS sequence is to preserve the alignment of the -LLLLGAGE- (SEQ ID NO:130) sequence motif.

Page 98 of the specification, beginning at line 27 and ending at line 37, has been amended as follows:

Random oligonucleotides to be expressed by the expression plasmid CADUS 1215 will encode tridecapeptides constructed as 5'

CGTGAAGCTTAAGCGTGAGGCAGAAGCT (NNK)13TGATCATCCG, (SEQ ID NO:6) where N is any nucleotide, K is either T or G at a ratio of 40:60 (see Proc Natl Acad Sci 87:6378, 1990; *ibid* 89:5393, 1992), and the AflII and BclI sites are underlined. This oligonucleotide is designed such that: the AflII and BclI sites permit inserting the oligos into the AflII and BglII site of CADUS 1215 (see Figure 4); the HindIII site just 5' to the AflII site in the 5' end of the oligo allows future flexibility with cloning of the oligos; the virtual repeat of GAGGCT (SEQ ID NO:131) and the GAGA (SEQ ID NO:132) repeats which

Page 101 of the specification, beginning at line 10 and ending at line 12, has been amended as follows:

Clearly, these sequences encode novel peptides, as the native **a**-factor sequence differs considerably: Tyr Ile Ile Lys Gly Val Phe Trp Asp Pro Ala (SEQ ID NO:133).

Appendix B
CLEAN VERSION

Page 6 of the specification, beginning at line 1 and ending at line 9, as amended will read as follows:

on expression of the transcription factor STE12. STE12 stimulates expression of a wide variety of genes involved in mating, including FUS1 (cell fusion), FAR1 (cell-cycle arrest), STE2 (the receptor), MFA1 (the pheromone), SST2 (recovery), KAR3 (nuclear fusion) and STE6 (pheromone secretion). Other genes activated by the pathway are CHS1, AGα1, and KAR3. The multiply tandem sequence TGAAACA (SEQ ID NO:128) has been recognized as a "pheromone response element" found in the 5'-flanking regions of many of the genes of this pathway.

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